

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

## SEQUENCE LISTING

<110> Sims, John  
Born, Theresa

<120> ACPL DNA and Polypeptides

<130> 2872-US

<140> 09/616,530

<141> 2000-07-14

<150> PCT/US99/01420

<151> 1999-01-22

<150> 60/078,835

<151> 1998-03-20

<150> 60/072,301

<151> 1998-01-23

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 1845

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (1)..(1845)

<223>

<400> 1	
atg ctc tgt ttg ggc tgg gtg ttt ctt tgg ttt gtt gca gga gag aag	48
Met Leu Cys Leu Gly Trp Val Phe Leu Trp Phe Val Ala Gly Glu Lys	
1 5 10 15	
acc aca gga ttt aat cat tca gct tgt gcc acc aaa aaa ctt ctg tgg	96
Thr Thr Gly Phe Asn His Ser Ala Cys Ala Thr Lys Lys Leu Leu Trp	
20 25 30	
aca tat tct gca agg ggt gca gag aat ttt gtc cta ttt tgt gac tta	144
Thr Tyr Ser Ala Arg Gly Ala Glu Asn Phe Val Leu Phe Cys Asp Leu	
35 40 45	
caa gag ctt cag gag caa aaa ttc tcc cat gca agt caa ctg tca cca	192
Gln Glu Leu Gln Glu Gln Lys Phe Ser His Ala Ser Gln Leu Ser Pro	
50 55 60	
aca caa agt cct gct cac aaa cct tgc agt ggc agt cag aag gac cta	240
Thr Gln Ser Pro Ala His Lys Pro Cys Ser Gly Ser Gln Lys Asp Leu	
65 70 75 80	
tct gat gtc cag tgg tac atg caa cct cgg agt gga agt cca cta gag	288
Ser Asp Val Gln Trp Tyr Met Gln Pro Arg Ser Gly Ser Pro Leu Glu	
85 90 95	

gag atc agt aga aac tct ccc cat atg cag agt gaa ggc atg ctg cat	336
Glu Ile Ser Arg Asn Ser Pro His Met Gln Ser Glu Gly Met Leu His	
100 105 110	
ata ttg gcc cca cag acg aac agc att tgg tca tat att tgt aga ccc	384
Ile Leu Ala Pro Gln Thr Asn Ser Ile Trp Ser Tyr Ile Cys Arg Pro	
115 120 125	
aga att agg agc ccc cag gat atg gcc tgt tgt atc aag aca gtc tta	432
Arg Ile Arg Ser Pro Gln Asp Met Ala Cys Cys Ile Lys Thr Val Leu	
130 135 140	
gaa gtt aag cct cag aga aac gtg tcc tgt ggg aac aca gca caa gat	480
Glu Val Lys Pro Gln Arg Asn Val Ser Cys Gly Asn Thr Ala Gln Asp	
145 150 155 160	
gaa caa gtc cta ctt ctt ggc agt act ggc tcc att cat tgt ccc agt	528
Glu Gln Val Leu Leu Leu Gly Ser Thr Gly Ser Ile His Cys Pro Ser	
165 170 175	
ctc agc tgc caa agt gat gta cag agt cca gag atg acc tgg tac aag	576
Leu Ser Cys Gln Ser Asp Val Gln Ser Pro Glu Met Thr Trp Tyr Lys	
180 185 190	
gat gga aga cta ctt cct gag cac aag aaa aat cca att gag atg gca	624
Asp Gly Arg Leu Leu Pro Glu His Lys Lys Asn Pro Ile Glu Met Ala	
195 200 205	
gat att tat gtt ttt aat caa ggc ttg tat gta tgt gat tac aca cag	672
Asp Ile Tyr Val Phe Asn Gln Gly Leu Tyr Val Cys Asp Tyr Thr Gln	
210 215 220	
tca gat aat gtg agt tcc tgg aca gtc cga gct gtg gtt aaa gtg aga	720
Ser Asp Asn Val Ser Ser Trp Thr Val Arg Ala Val Val Lys Val Arg	
225 230 235 240	
acc att ggt aag gac atc aat gtg aag ccg gaa att ctg gat ccc att	768
Thr Ile Gly Lys Asp Ile Asn Val Lys Pro Glu Ile Leu Asp Pro Ile	
245 250 255	
aca gat aca ctg gac gta gag ctt gga aag cct tta act ctc ccc tgc	816
Thr Asp Thr Leu Asp Val Glu Leu Gly Lys Pro Leu Thr Leu Pro Cys	
260 265 270	
aga gta cag ttt ggc ttc caa aga ctt tca aag cct gtg ata aag tgg	864
Arg Val Gln Phe Gly Phe Gln Arg Leu Ser Lys Pro Val Ile Lys Trp	
275 280 285	
tat gtc aaa gaa tct aca cag gag tgg gaa atg tca gta ttt gag gag	912
Tyr Val Lys Glu Ser Thr Gln Glu Trp Glu Met Ser Val Phe Glu Glu	
290 295 300	
aaa aga att caa tcc act ttc aag aat gaa gtc att gaa cgt acc atc	960
Lys Arg Ile Gln Ser Thr Phe Lys Asn Glu Val Ile Glu Arg Thr Ile	
305 310 315 320	
ttc ttg aga gaa gtt acc cag aga gat ctc agc aga aag ttt gtt tgc	1008
Phe Leu Arg Glu Val Thr Gln Arg Asp Leu Ser Arg Lys Phe Val Cys	
325 330 335	
ttt gcc cag aac tcc att ggg aac aca aca cgg acc ata cgg ctg agg	1056

Phe	Ala	Gln	Asn	Ser	Ile	Gly	Asn	Thr	Thr	Arg	Thr	Ile	Arg	Leu	Arg		
			340					345					350				
aag	aag	gaa	gag	gtg	gtg	ttt	gta	tac	atc	ctt	ctc	ggc	acg	gcc	ttg	1104	
Lys	Lys	Glu	Glu	Val	Val	Phe	Val	Tyr	Ile	Leu	Leu	Gly	Thr	Ala	Leu		
		355					360					365					
atg	ctg	gtg	ggc	gtt	ctg	gtg	gca	gct	gct	ttc	ctc	tac	tgg	tac	tgg	1152	
Met	Leu	Val	Gly	Val	Leu	Val	Ala	Ala	Ala	Phe	Leu	Tyr	Trp	Tyr	Trp		
	370					375					380						
att	gaa	gtt	gtc	ctg	ctc	tgt	cga	acc	tac	aag	aac	aaa	gat	gag	act	1200	
Ile	Glu	Val	Val	Leu	Leu	Cys	Arg	Thr	Tyr	Lys	Asn	Lys	Asp	Glu	Thr		
385					390					395					400		
ctg	ggg	gat	aag	aag	gaa	ttc	gat	gca	ttt	gta	tcc	tac	tcg	aat	tgg	1248	
Leu	Gly	Asp	Lys	Lys	Glu	Phe	Asp	Ala	Phe	Val	Ser	Tyr	Ser	Asn	Trp		
				405					410					415			
agc	tct	cct	gag	act	gac	gcc	gtg	gga	tct	ctg	agt	gag	gaa	cac	ctg	1296	
Ser	Ser	Pro	Glu	Thr	Asp	Ala	Val	Gly	Ser	Leu	Ser	Glu	Glu	His	Leu		
			420					425					430				
gct	ctg	aat	ctt	ttc	ccg	gaa	gtg	cta	gaa	gac	acc	tat	ggg	tac	aga	1344	
Ala	Leu	Asn	Leu	Phe	Pro	Glu	Val	Leu	Glu	Asp	Thr	Tyr	Gly	Tyr	Arg		
		435				440						445					
ttg	tgt	ttg	ctt	gac	cga	gat	gtg	acc	cca	gga	gga	gtg	tat	gca	gat	1392	
Leu	Cys	Leu	Leu	Asp	Arg	Asp	Val	Thr	Pro	Gly	Gly	Val	Tyr	Ala	Asp		
	450					455					460						
gac	att	gtg	agc	atc	att	aag	aaa	agc	cga	aga	gga	ata	ttt	atc	ctg	1440	
Asp	Ile	Val	Ser	Ile	Ile	Lys	Lys	Ser	Arg	Arg	Gly	Ile	Phe	Ile	Leu		
465					470				475						480		
agt	ccc	agc	tac	ctc	aat	gga	ccc	cgt	gtc	ttt	gag	cta	caa	gca	gca	1488	
Ser	Pro	Ser	Tyr	Leu	Asn	Gly	Pro	Arg	Val	Phe	Glu	Leu	Gln	Ala	Ala		
				485				490					495				
gtg	aat	ctt	gcc	ttg	gtt	gat	cag	aca	ctg	aag	ttg	att	tta	att	aag	1536	
Val	Asn	Leu	Ala	Leu	Val	Asp	Gln	Thr	Leu	Lys	Leu	Ile	Leu	Ile	Lys		
			500					505					510				
ttc	tgt	tcc	ttc	caa	gag	cca	gaa	tct	ctt	cct	tac	ctt	gtc	aaa	aag	1584	
Phe	Cys	Ser	Phe	Gln	Glu	Pro	Glu	Ser	Leu	Pro	Tyr	Leu	Val	Lys	Lys		
		515					520					525					
gct	ctg	cgg	gtt	ctc	ccc	aca	gtc	aca	tgg	aaa	ggc	ttg	aag	tcg	gtc	1632	
Ala	Leu	Arg	Val	Leu	Pro	Thr	Val	Thr	Trp	Lys	Gly	Leu	Lys	Ser	Val		
	530					535					540						
cac	gcc	agt	tcc	agg	ttc	tgg	acc	caa	att	cgt	tac	cac	atg	cct	gtg	1680	
His	Ala	Ser	Ser	Arg	Phe	Trp	Thr	Gln	Ile	Arg	Tyr	His	Met	Pro	Val		
545					550					555					560		
aag	aac	tcc	aac	agg	ttt	atg	ttc	aac	ggg	ctc	aga	att	ttc	ctg	aag	1728	
Lys	Asn	Ser	Asn	Arg	Phe	Met	Phe	Asn	Gly	Leu	Arg	Ile	Phe	Leu	Lys		
				565					570					575			
ggc	ttt	tcc	cct	gaa	aag	gac	cta	gtg	aca	cag	aaa	ccc	ctg	gaa	gga	1776	
Gly	Phe	Ser	Pro	Glu	Lys	Asp	Leu	Val	Thr	Gln	Lys	Pro	Leu	Glu	Gly		

580	585	590	
atg ccc aag tct ggg aat gac cac gga gct cag aac ctc ctt ctc tac			1824
Met Pro Lys Ser Gly Asn Asp His Gly Ala Gln Asn Leu Leu Leu Tyr			
595	600	605	
agt gac cag aag agg tgc tga			1845
Ser Asp Gln Lys Arg Cys			
610			
<210> 2			
<211> 614			
<212> PRT			
<213> Mus sp.			
<400> 2			
Met Leu Cys Leu Gly Trp Val Phe Leu Trp Phe Val Ala Gly Glu Lys			
1	5	10	15
Thr Thr Gly Phe Asn His Ser Ala Cys Ala Thr Lys Lys Leu Leu Trp			
	20	25	30
Thr Tyr Ser Ala Arg Gly Ala Glu Asn Phe Val Leu Phe Cys Asp Leu			
	35	40	45
Gln Glu Leu Gln Glu Gln Lys Phe Ser His Ala Ser Gln Leu Ser Pro			
	50	55	60
Thr Gln Ser Pro Ala His Lys Pro Cys Ser Gly Ser Gln Lys Asp Leu			
65	70	75	80
Ser Asp Val Gln Trp Tyr Met Gln Pro Arg Ser Gly Ser Pro Leu Glu			
	85	90	95
Glu Ile Ser Arg Asn Ser Pro His Met Gln Ser Glu Gly Met Leu His			
	100	105	110
Ile Leu Ala Pro Gln Thr Asn Ser Ile Trp Ser Tyr Ile Cys Arg Pro			
	115	120	125
Arg Ile Arg Ser Pro Gln Asp Met Ala Cys Cys Ile Lys Thr Val Leu			
	130	135	140
Glu Val Lys Pro Gln Arg Asn Val Ser Cys Gly Asn Thr Ala Gln Asp			
145	150	155	160
Glu Gln Val Leu Leu Leu Gly Ser Thr Gly Ser Ile His Cys Pro Ser			
	165	170	175

Leu Ser Cys Gln Ser Asp Val Gln Ser Pro Glu Met Thr Trp Tyr Lys  
180 185 190

Asp Gly Arg Leu Leu Pro Glu His Lys Lys Asn Pro Ile Glu Met Ala  
195 200 205

Asp Ile Tyr Val Phe Asn Gln Gly Leu Tyr Val Cys Asp Tyr Thr Gln  
210 215 220

Ser Asp Asn Val Ser Ser Trp Thr Val Arg Ala Val Val Lys Val Arg  
225 230 235 240

Thr Ile Gly Lys Asp Ile Asn Val Lys Pro Glu Ile Leu Asp Pro Ile  
245 250 255

Thr Asp Thr Leu Asp Val Glu Leu Gly Lys Pro Leu Thr Leu Pro Cys  
260 265 270

Arg Val Gln Phe Gly Phe Gln Arg Leu Ser Lys Pro Val Ile Lys Trp  
275 280 285

Tyr Val Lys Glu Ser Thr Gln Glu Trp Glu Met Ser Val Phe Glu Glu  
290 295 300

Lys Arg Ile Gln Ser Thr Phe Lys Asn Glu Val Ile Glu Arg Thr Ile  
305 310 315 320

Phe Leu Arg Glu Val Thr Gln Arg Asp Leu Ser Arg Lys Phe Val Cys  
325 330 335

Phe Ala Gln Asn Ser Ile Gly Asn Thr Thr Arg Thr Ile Arg Leu Arg  
340 345 350

Lys Lys Glu Glu Val Val Phe Val Tyr Ile Leu Leu Gly Thr Ala Leu  
355 360 365

Met Leu Val Gly Val Leu Val Ala Ala Ala Phe Leu Tyr Trp Tyr Trp  
370 375 380

Ile Glu Val Val Leu Leu Cys Arg Thr Tyr Lys Asn Lys Asp Glu Thr  
385 390 395 400

Leu Gly Asp Lys Lys Glu Phe Asp Ala Phe Val Ser Tyr Ser Asn Trp  
405 410 415

Ser Ser Pro Glu Thr Asp Ala Val Gly Ser Leu Ser Glu Glu His Leu  
 420 425 430

Ala Leu Asn Leu Phe Pro Glu Val Leu Glu Asp Thr Tyr Gly Tyr Arg  
 435 440 445

Leu Cys Leu Leu Asp Arg Asp Val Thr Pro Gly Gly Val Tyr Ala Asp  
 450 455 460

Asp Ile Val Ser Ile Ile Lys Lys Ser Arg Arg Gly Ile Phe Ile Leu  
 465 470 475 480

Ser Pro Ser Tyr Leu Asn Gly Pro Arg Val Phe Glu Leu Gln Ala Ala  
 485 490 495

Val Asn Leu Ala Leu Val Asp Gln Thr Leu Lys Leu Ile Leu Ile Lys  
 500 505 510

Phe Cys Ser Phe Gln Glu Pro Glu Ser Leu Pro Tyr Leu Val Lys Lys  
 515 520 525

Ala Leu Arg Val Leu Pro Thr Val Thr Trp Lys Gly Leu Lys Ser Val  
 530 535 540

His Ala Ser Ser Arg Phe Trp Thr Gln Ile Arg Tyr His Met Pro Val  
 545 550 555 560

Lys Asn Ser Asn Arg Phe Met Phe Asn Gly Leu Arg Ile Phe Leu Lys  
 565 570 575

Gly Phe Ser Pro Glu Lys Asp Leu Val Thr Gln Lys Pro Leu Glu Gly  
 580 585 590

Met Pro Lys Ser Gly Asn Asp His Gly Ala Gln Asn Leu Leu Leu Tyr  
 595 600 605

Ser Asp Gln Lys Arg Cys  
 610

<210> 3  
 <211> 754  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (6)..(8)  
 <223> "n" = a, t, c, g

<220>  
 <221> misc\_feature  
 <222> (563)..(563)  
 <223> "n" = a, t, c, g

<220>  
 <221> misc\_feature  
 <222> (596)..(596)  
 <223> "n" = a, t, c, g

<220>  
 <221> misc\_feature  
 <222> (607)..(607)  
 <223> "n" = a, t, c, g

<220>  
 <221> misc\_feature  
 <222> (708)..(708)  
 <223> "n" = a, t, c, g

<220>  
 <221> misc\_feature  
 <222> (729)..(729)  
 <223> "n" = a, t, c, g

<220>  
 <221> misc\_feature  
 <222> (752)..(752)  
 <223> "n" = a, t, c, g

<400> 3  
 tggggnnntg gacagacact gctggcatat ttgtggcaag aagttgatgg ataaaattgt 60  
 taattaagga ctggactctt ctttatTTtg aaataaacca tgagtTTaag gatggagggg 120  
 tggactcgga tatgcttgac ttgcacagtt tcttgggtgg attctccttt cagttcaatt 180  
 actcagccag atggcaccac aaagaaatct tgtgggaaaa gacagggata ggagctcagg 240  
 tctgcaaggg gcaggattag tgtgaaagag aatgcacaca agcagatatg gatcaattaa 300  
 caactaatgt tttaccagca cccacaacct gatgtggcag tcatttttagg gggcaagctt 360  
 tttacatgga aaccggaatt cctaacttac aggtaattag taaaatgtga agacagaact 420  
 ccaagacatt tagatcaaag tgtggctgtg cacctaaatc ttcataaagc aggccttcag 480  
 actttccaat gcaaatagta atctttgttt tcattcttca gtgggagaca ctaaactcaa 540  
 accagatatt ctggattctg tcnaggacac actgggaagt agaacttgga aagcctntaa 600  
 ctattanctg caaagcacga tttggctttt aaagggtcct taaccctgtc ataaaatggt 660



acatcaaaga ttctgaccta aaatgggaaa tctcaatacc tgaaggcnaa aaagttttaa 720  
aatcccacnt ttaaaggatt aaaatcattg ancc 754

<210> 4  
<211> 523  
<212> DNA  
<213> Homo sapiens

<400> 4  
gtaaaatact caagcttttt acatgggaaac cggaattcct aacttacagg taattagtaa 60  
aatgtgaaga cagagctcca agacatttag atcaaagtgt ggctgtgcac ctaaattcttc 120  
atcaagcagg ccttcagact ttccaatgca aatagtaatc tttgttttca tctttcagtg 180  
ggagacacta aactcaaacc agatattctg gatcctgtcg aggacacact ggaagtagaa 240  
cttggtgaagc tgggcctcat cgcctttgaa tgacatcgtg ctgctgggag caggtctaag 300  
tgtgatagaa ggaaaacagc attgggattt ccagtcaaac agaattgggt gtgaatctta 360  
actcagccat tgactagttt tgtgactttg cacagttact tcatacttta agcctcagta 420  
cttagatccg caaatagcta tcataaaact gagcctaaaa gattatattg caggccgggc 480  
atggtggcct aagcctgtaa tcccagcact ttgggaggct gag 523

<210> 5  
<211> 22  
<212> PRT  
<213> Homo sapiens

<400> 5  
Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp Pro Val Glu Asp  
1 5 10 15

Thr Leu Glu Val Glu Leu  
20

<210> 6  
<211> 2681  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (484)..(2283)  
<223>

<400> 6  
ctctctggat aggaagaaat atagtagaac cctttgaaaa tggatatttt cacatatttt 60  
cgttcagata caaaagctgg cagttactga aataaggact tgaagttcct tcctcttttt 120

ttatgtctta agagcaggaa ataaagagac agctgaaggt gtagccttga ccaactgaaa	180
gggaaatctt catcctctga aaaaacatat gtgattctca aaaaacgcat ctggaaaatt	240
gataaagaag cgattctgta gattctccca gcgctgttgg gctctcaatt ccttctgtga	300
aggacaacat atggtgatgg ggaaatcaga agctttgaga ccctctacac ctggatatga	360
atcccccttc taatacttac cagaaatgaa ggggatactc agggcagagt tctgaatctc	420
aaaacactct actctggcaa aggaatgaag ttattggagt gatgacagga acacgggaga	480
aca atg ctc tgt ttg ggc tgg ata ttt ctt tgg ctt gtt gca gga gag	528
Met Leu Cys Leu Gly Trp Ile Phe Leu Trp Leu Val Ala Gly Glu	
1 5 10 15	
cga att aaa gga ttt aat att tca ggt tgt tcc aca aaa aaa ctc ctt	576
Arg Ile Lys Gly Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu	
20 25 30	
tgg aca tat tct aca agg agt gaa gag gaa ttt gtc tta ttt tgt gat	624
Trp Thr Tyr Ser Thr Arg Ser Glu Glu Glu Phe Val Leu Phe Cys Asp	
35 40 45	
tta cca gag cca cag aaa tca cat ttc tgc cac aga aat cga ctc tca	672
Leu Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser	
50 55 60	
cca aaa caa gtc cct gag cac ctg ccc ttc atg ggt agt aac gac cta	720
Pro Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu	
65 70 75	
tct gat gtc caa tgg tac caa caa cct tcg aat gga gat cca tta gag	768
Ser Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu	
80 85 90 95	
gac att agg aaa agc tat cct cac atc att cag gac aaa tgt acc ctt	816
Asp Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu	
100 105 110	
cac ttt ttg acc cca ggg gtg aat aat tct ggg tca tat att tgt aga	864
His Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg	
115 120 125	
ccc aag atg att aag agc ccc tat gat gta gcc tgt tgt gtc aag atg	912
Pro Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met	
130 135 140	
att tta gaa gtt aag ccc cag aca aat gca tcc tgt gag tat tcc gca	960
Ile Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala	
145 150 155	
tca cat aag caa gac cta ctt ctt ggg agc act ggc tct att tct tgc	1008
Ser His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys	
160 165 170 175	
ccc agt ctc agc tgc caa agt gat gca caa agt cca gcg gta acc tgg	1056
Pro Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp	
180 185 190	
tac aag aat gga aaa ctc ctc tct gtg gaa agg agc aac cga atc gta	1104

Tyr	Lys	Asn	Gly	Lys	Leu	Leu	Ser	Val	Glu	Arg	Ser	Asn	Arg	Ile	Val	
			195					200					205			
gtg	gat	gaa	gtt	tat	gac	tat	cac	cag	ggc	aca	tat	gta	tgt	gat	tac	1152
Val	Asp	Glu	Val	Tyr	Asp	Tyr	His	Gln	Gly	Thr	Tyr	Val	Cys	Asp	Tyr	
		210					215					220				
act	cag	tcg	gat	act	gtg	agt	tcg	tgg	aca	gtc	aga	gct	gtt	gtt	caa	1200
Thr	Gln	Ser	Asp	Thr	Val	Ser	Ser	Trp	Thr	Val	Arg	Ala	Val	Val	Gln	
	225					230					235					
gtg	aga	acc	att	gtg	gga	gac	act	aaa	ctc	aaa	cca	gat	att	ctg	gat	1248
Val	Arg	Thr	Ile	Val	Gly	Asp	Thr	Lys	Leu	Lys	Pro	Asp	Ile	Leu	Asp	
240					245					250					255	
cct	gtc	gag	gac	aca	ctg	gaa	gta	gaa	ctt	gga	aag	cct	tta	act	att	1296
Pro	Val	Glu	Asp	Thr	Leu	Glu	Val	Glu	Leu	Gly	Lys	Pro	Leu	Thr	Ile	
				260					265					270		
agc	tgc	aaa	gca	cga	ttt	ggc	ttt	gaa	agg	gtc	ttt	aac	cct	gtc	ata	1344
Ser	Cys	Lys	Ala	Arg	Phe	Gly	Phe	Glu	Arg	Val	Phe	Asn	Pro	Val	Ile	
			275					280					285			
aaa	tgg	tac	atc	aaa	gat	tct	gac	cta	gag	tgg	gaa	gtc	tca	gta	cct	1392
Lys	Trp	Tyr	Ile	Lys	Asp	Ser	Asp	Leu	Glu	Trp	Glu	Val	Ser	Val	Pro	
		290					295					300				
gag	gcg	aaa	agt	att	aaa	tcc	act	tta	aag	gat	gaa	atc	att	gag	cgt	1440
Glu	Ala	Lys	Ser	Ile	Lys	Ser	Thr	Leu	Lys	Asp	Glu	Ile	Ile	Glu	Arg	
	305					310					315					
aat	atc	atc	ttg	gaa	aaa	gtc	act	cag	cgt	gat	ctt	cgc	agg	aag	ttt	1488
Asn	Ile	Ile	Leu	Glu	Lys	Val	Thr	Gln	Arg	Asp	Leu	Arg	Arg	Lys	Phe	
320					325					330					335	
gtt	tgc	ttt	gtc	cag	aac	tcc	att	gga	aac	aca	acc	cag	tcc	gtc	caa	1536
Val	Cys	Phe	Val	Gln	Asn	Ser	Ile	Gly	Asn	Thr	Thr	Gln	Ser	Val	Gln	
				340					345					350		
ctg	aaa	gaa	aag	aga	gga	gtg	gtg	ctc	ctg	tac	atc	ctg	ctt	ggc	acc	1584
Leu	Lys	Glu	Lys	Arg	Gly	Val	Val	Leu	Leu	Tyr	Ile	Leu	Leu	Gly	Thr	
			355					360					365			
atc	ggg	acc	ctg	gtg	gcc	gtg	ctg	gcg	gcg	agt	gcc	ctc	ctc	tac	agg	1632
Ile	Gly	Thr	Leu	Val	Ala	Val	Leu	Ala	Ala	Ser	Ala	Leu	Leu	Tyr	Arg	
		370					375					380				
cac	tgg	att	gaa	ata	gtg	ctg	ctg	tac	cgg	acc	tac	cag	agc	aag	gat	1680
His	Trp	Ile	Glu	Ile	Val	Leu	Leu	Tyr	Arg	Thr	Tyr	Gln	Ser	Lys	Asp	
	385					390					395					
cag	acg	ctt	ggg	gat	aaa	aag	gat	ttt	gat	gct	ttc	gta	tcc	tat	gca	1728
Gln	Thr	Leu	Gly	Asp	Lys	Lys	Asp	Phe	Asp	Ala	Phe	Val	Ser	Tyr	Ala	
400					405				410						415	
aaa	tgg	agc	tct	ttt	cca	agt	gag	gcc	act	tca	tct	ctg	agt	gaa	gaa	1776
Lys	Trp	Ser	Ser	Phe	Pro	Ser	Glu	Ala	Thr	Ser	Ser	Leu	Ser	Glu	Glu	
				420					425					430		
cac	ttg	gcc	ctg	agc	cta	ttt	cct	gat	gtt	tta	gaa	aac	aaa	tat	gga	1824
His	Leu	Ala	Leu	Ser	Leu	Phe	Pro	Asp	Val	Leu	Glu	Asn	Lys	Tyr	Gly	

435	440	445	
tat agc ctg tgt ttg ctt gaa aga gat gtg gct cca gga gga gtg tat			1872
Tyr Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr			
450	455	460	
gca gaa gac att gtg agc att att aag aga agc aga gga ata ttt			1920
Ala Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe			
465	470	475	
atc ttg agc ccc aac tat gtc aat gga ccc agt atc ttt gaa cta caa			1968
Ile Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln			
480	485	490	495
gca gca gtg aat ctt gcc ttg gat gat caa aca ctg aaa ctc att tta			2016
Ala Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu			
	500	505	510
att aag ttc tgt tac ttc caa gag cca gag tct cta cct cat ctc gtg			2064
Ile Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val			
	515	520	525
aaa aaa gct ctc agg gtt ttg ccc aca gtt act tgg aga ggc tta aaa			2112
Lys Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys			
	530	535	540
tca gtt cct ccc aat tct agg ttc tgg gcc aaa atg cgc tac cac atg			2160
Ser Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met			
	545	550	555
cct gtg aaa aac tct cag gga ttc acg tgg aac cag ctc aga att acc			2208
Pro Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr			
560	565	570	575
tct agg att ttt cag tgg aaa gga ctc agt aga aca gaa acc act ggg			2256
Ser Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly			
	580	585	590
agg agc tcc cag cct aag gaa tgg tga aatgagccct ggagccccct			2303
Arg Ser Ser Gln Pro Lys Glu Trp			
	595		
ccagtccagt ccctgggata gagatgttgc tggacagaac tcacagctct gtgtgtgtgt			2363
gttcaggctg ataggaaatt caaagagtct cctgccagca ccaagcaagc ttgatggaca			2423
atggaatggg attgagactg tggtttagag cctttgattt cctggactgg acagacggcg			2483
agtgaattct ctagaccttg ggtactttca gtacacaaca cccctaagat ttcccagtgg			2543
tccgagcaga atcagaaaat acagctactt ctgccttatg gctaggggaac tgtcatgtct			2603
accatgtatt gtacatatga ctttatgtat acttgcaatc aaataaatat tattttatta			2663
gaaaaaaaaac cggaattc			2681

<210> 7  
 <211> 599  
 <212> PRT  
 <213> Homo sapiens

<400> 7

Met Leu Cys Leu Gly Trp Ile Phe Leu Trp Leu Val Ala Gly Glu Arg  
1 5 10 15

Ile Lys Gly Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu Trp  
20 25 30

Thr Tyr Ser Thr Arg Ser Glu Glu Glu Phe Val Leu Phe Cys Asp Leu  
35 40 45

Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser Pro  
50 55 60

Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu Ser  
65 70 75 80

Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu Asp  
85 90 95

Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu His  
100 105 110

Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg Pro  
115 120 125

Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met Ile  
130 135 140

Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala Ser  
145 150 155 160

His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys Pro  
165 170 175

Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp Tyr  
180 185 190

Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val Val  
195 200 205

Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr Thr  
210 215 220

Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln Val  
225 230 235 240

Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp Pro  
 245 250 255

Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile Ser  
 260 265 270

Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile Lys  
 275 280 285

Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro Glu  
 290 295 300

Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg Asn  
 305 310 315 320

Ile Ile Leu Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe Val  
 325 330 335

Cys Phe Val Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln Leu  
 340 345 350

Lys Glu Lys Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr Ile  
 355 360 365

Gly Thr Leu Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg His  
 370 375 380

Trp Ile Glu Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp Gln  
 385 390 395 400

Thr Leu Gly Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala Lys  
 405 410 415

Trp Ser Ser Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu His  
 420 425 430

Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly Tyr  
 435 440 445

Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr Ala  
 450 455 460

Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe Ile  
 465 470 475 480

Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln Ala  
485 490 495

Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu Ile  
500 505 510

Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val Lys  
515 520 525

Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys Ser  
530 535 540

Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met Pro  
545 550 555 560

Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr Ser  
565 570 575

Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly Arg  
580 585 590

Ser Ser Gln Pro Lys Glu Trp  
595